

WO 01/04326

PCT/EP00/06609

SEQUENCE LISTING

<110> Pharmacia & Upjohn S.p.A, et al

<120> Tankyrase Homolog Protein (THP), Nucleic Acids, and
Methods Related To The Same

<130> REP06471WO

<140> not yet known

<141> 2000-07-03

<150> 09/350,982

<151> 1999-07-09

<160> 10

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<213> Homo sapien

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gtg aac agc cgc gac acg gcg gcc agg aaa tcc acc ccg ctg cac ctc	192
Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu	
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ggt gca aat gtc caa gca cgt gat gat ggg gcc ctt att cct ctt cat	288
Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His	
85 90 95	
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Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg	
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His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu	
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cat gaa gct gca att aaa gga aag att gat gtt tgc att gtg ctg tta	432
His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu	
130 135 140	
cag cat gga gct gag cca acc atc cga aat aca gat gga agg aca gca	480
Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala	
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Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys	
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Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala	
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Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr	
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Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu	
325 330 335	
caa gct gca cga gaa gct gat gtt act cga atc aaa aaa cat ctc tct	1056
Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser	
340 345 350	
ctg gaa atg gtg aat ttc aag cat cct caa aca cat gaa aca gca ntg	1104
Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Xaa	
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cat tgt gct gct gca tct cca tat ccc aaa aga aag caa ata tgt gaa	1152
His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu	
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Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr	
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Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu	
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act gtt cag agt gtc aac tgc aga gac att gaa ggg cgt cag tct aca	1584
Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr	
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Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr	
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Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu	
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 Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys
 595 600 605

aaa ctt ctg ctc cag cat ggt gca gac cct aca aaa aaa aac agg gat 1872
 Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp
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 Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln
 625 630 635 640

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 Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys
 660 665 670

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 675 680 685

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 690 695 700

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 Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala
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 Cys Val Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala
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gcc caa aag gga cga aca cag ctt tgt gct ttg ktg cta gcc cat gga 2304
 Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Xaa Leu Ala His Gly
 755 760 765

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Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys	
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980 985 990	
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Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg	
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Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala	
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Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly	
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1140 1145 1150	

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att act tac cag att atg agg cct gaa ggt atg gtc gat gga 3498
 Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val Asp Gly
 1155 1160 1165

<210> 5

<211> 1166

<212> PRT

<213> Homo sapiens

<400> 5

Met Ser Gly Arg Arg Cys Ala Gly Gly Gly Ala Ala Cys Ala Ser Ala
 1 5 10 15

Ala Ala Glu Ala Val Glu Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys
 20 25 30

Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys
 35 40 45

Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu
 50 55 60

Ala Ala Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn
 65 70 75 80

Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His
 85 90 95

Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg
 100 105 110

His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu
 115 120 125

His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu
 130 135 140

Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala
 145 150 155 160

Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr
 165 170 175

Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys
 180 185 190

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Met	Met	Ala	Leu	Leu	Thr	Pro	Leu	Asn	Val	Asn	Cys	His	Ala	Ser	Asp
		195					200					205			
Gly	Arg	Lys	Ser	Thr	Pro	Leu	His	Leu	Ala	Ala	Gly	Tyr	Asn	Arg	Val
	210					215					220				
Lys	Ile	Val	Gln	Leu	Leu	Leu	Gln	His	Gly	Ala	Asp	Val	His	Ala	Lys
225					230					235					240
Asp	Lys	Gly	Asp	Leu	Val	Pro	Leu	His	Asn	Ala	Cys	Ser	Tyr	Gly	His
				245					250					255	
Tyr	Glu	Val	Thr	Glu	Leu	Leu	Val	Lys	His	Gly	Ala	Cys	Val	Asn	Ala
			260					265						270	
Met	Asp	Leu	Trp	Gln	Phe	Thr	Pro	Leu	His	Glu	Ala	Ala	Ser	Lys	Asn
		275					280						285		
Arg	Val	Glu	Val	Cys	Ser	Leu	Leu	Leu	Ser	Tyr	Gly	Ala	Asp	Pro	Thr
	290					295					300				
Leu	Leu	Asn	Cys	His	Asn	Lys	Ser	Ala	Ile	Asp	Leu	Ala	Pro	Thr	Pro
305					310					315					320
Gln	Leu	Lys	Glu	Arg	Leu	Ala	Tyr	Glu	Phe	Lys	Gly	His	Ser	Leu	Leu
				325					330					335	
Gln	Ala	Ala	Arg	Glu	Ala	Asp	Val	Thr	Arg	Ile	Lys	Lys	His	Leu	Ser
			340					345					350		
Leu	Glu	Met	Val	Asn	Phe	Lys	His	Pro	Gln	Thr	His	Glu	Thr	Ala	Xaa
		355					360					365			
His	Cys	Ala	Ala	Ala	Ser	Pro	Tyr	Pro	Lys	Arg	Lys	Gln	Ile	Cys	Glu
	370					375					380				
Leu	Leu	Leu	Arg	Lys	Gly	Ala	Xaa	Ile	Asn	Glu	Lys	Thr	Lys	Glu	Phe
385					390					395					400
Leu	Thr	Pro	Leu	His	Val	Ala	Ser	Glu	Lys	Ala	His	Asn	Asp	Xaa	Val
				405					410					415	
Glu	Val	Val	Val	Lys	His	Glu	Ala	Lys	Val	Asn	Ala	Leu	Asp	Asn	Leu
			420					425					430		
Gly	Gln	Thr	Ser	Leu	His	Arg	Ala	Ala	Tyr	Cys	Gly	His	Leu	Gln	Thr
		435					440					445			

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Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu
 450 455 460

Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu
 465 470 475 480

Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu
 485 490 495

Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys
 500 505 510

Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr
 515 520 525

Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr
 530 535 540

Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys Xaa Xaa Leu
 545 550 555 560

Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu
 565 570 575

Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys
 580 585 590

Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys
 595 600 605

Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp
 610 615 620

Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln
 625 630 635 640

Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Ser
 645 650 655

Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys
 660 665 670

Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly
 675 680 685

Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp
 690 695 700

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Val	Asn	Ala	Gln	Asp	Lys	Gly	Gly	Leu	Ile	Pro	Leu	His	Asn	Ala	Ala	
705					710					715					720	
Ser	Tyr	Gly	His	Val	Asp	Val	Ala	Ala	Leu	Leu	Ile	Lys	Tyr	Asn	Ala	
				725					730					735		
Cys	Val	Asn	Ala	Thr	Asp	Lys	Trp	Ala	Phe	Thr	Pro	Leu	His	Glu	Ala	
			740					745						750		
Ala	Gln	Lys	Gly	Arg	Thr	Gln	Leu	Cys	Ala	Leu	Xaa	Leu	Ala	His	Gly	
		755					760							765		
Ala	Asp	Pro	Thr	Leu	Lys	Asn	Gln	Glu	Gly	Gln	Thr	Pro	Leu	Asp	Leu	
	770					775					780					
Val	Ser	Ala	Asp	Asp	Val	Ser	Ala	Leu	Leu	Thr	Ala	Ala	Met	Pro	Pro	
785					790					795					800	
Ser	Ala	Leu	Pro	Ser	Cys	Tyr	Lys	Pro	Gln	Val	Leu	Asn	Gly	Val	Arg	
				805					810					815		
Ser	Pro	Gly	Ala	Thr	Ala	Asp	Ala	Leu	Ser	Ser	Gly	Pro	Ser	Ser	Pro	
			820					825					830			
Ser	Ser	Leu	Ser	Ala	Ala	Ser	Ser	Leu	Asp	Asn	Leu	Ser	Gly	Ser	Phe	
		835					840					845				
Ser	Glu	Leu	Ser	Ser	Val	Val	Ser	Ser	Ser	Gly	Thr	Glu	Gly	Ala	Ser	
	850					855					860					
Ser	Leu	Glu	Lys	Lys	Glu	Val	Pro	Gly	Val	Asp	Phe	Ser	Ile	Thr	Gln	
865					870					875					880	
Phe	Val	Arg	Xaa	Leu	Gly	Leu	Glu	His	Leu	Met	Asp	Ile	Phe	Glu	Arg	
				885					890					895		
Glu	Gln	Ile	Thr	Leu	Asp	Val	Leu	Val	Glu	Met	Gly	His	Lys	Glu	Leu	
			900					905					910			
Lys	Glu	Ile	Gly	Ile	Asn	Ala	Tyr	Gly	His	Arg	His	Lys	Leu	Ile	Lys	
		915					920					925				
Gly	Val	Glu	Arg	Leu	Ile	Ser	Gly	Gln	Gln	Gly	Leu	Asn	Pro	Tyr	Leu	
	930					935					940					
Thr	Leu	Asn	Thr	Ser	Gly	Ser	Gly	Thr	Ile	Leu	Ile	Asp	Leu	Ser	Pro	
945					950					955					960	

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Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val
 965 970 975

Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr
 980 985 990

Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg
 995 1000 1005

Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala
 1010 1015 1020

Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile Ile
 1025 1030 1035 1040

His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met Phe Gly
 1045 1050 1055

Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln Tyr Val
 1060 1065 1070

Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp Arg Ser
 1075 1080 1085

Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly
 1090 1095 1100

Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser Pro Pro
 1105 1110 1115 1120

Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu Ala Leu
 1125 1130 1135

Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr Pro Glu Tyr Leu
 1140 1145 1150

Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val Asp Gly
 1155 1160 1165

<210> 6

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primers

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<400> 6
cccgagagct gttcgaggc 19

<210> 7
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primers

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caatctttac tctgttatat cct 23

<210> 8
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primers

<400> 8
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<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primers

<400> 9
aaggatccac cataccttca ggcct 25

<210> 10
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primers

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<400> 10

aaaagcttta tggaaaggat catgtcgggt cgccgctgc

39